

Summary SEQ ID NO:1 against DNA db's

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 10:11:26 ; Search time 3098 Seconds
(without alignments)
10418.015 Million cell updates/sec

Title: US-09-941-936A-1
Perfect score: 1109
Sequence: 1 tggaactggtgctccgttgt.....gctcttcgaggtgcgcttcc 1109

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

Also searched SEQ ID NO:2
(the encoded amino acid seq) in
DNA db's - but all same hits.

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1109	100.0	1109	6	AX394571	AX394571 Sequence
c	2	1107.4	99.9	340000	1	AP005274	AP005274 Corynebact
c	3	1107.4	99.9	349980	6	AX120085	AX120085 Sequence
	4	577.4	52.1	579	6	AX120368	AX120368 Sequence
	5	161.4	14.6	17570	1	AE007063	AE007063 Mycobacte
	6	161.4	14.6	39430	1	MTCY49	Z73966 Mycobacteri
	7	161.4	14.6	318200	1	MLEPRTN6	AL583922 Mycobacte
c	8	157.2	14.2	20198	1	SCM2	AL136149 Streptomy
c	9	128	11.5	1603	6	AX066107	AX066107 Sequence
c	10	65.6	5.9	37049	1	MLACEA	Z46257 M.leprae ac
c	11	65.6	5.9	342300	1	MLEPRTN8	AL583924 Mycobacte
	12	60.6	5.5	32941	1	SCM10	AL133469 Streptomy
	13	59.8	5.4	323450	1	SME591790	AL591790 Sinorhizo
c	14	57.8	5.2	124501	2	AC118134	AC118134 Oryza sat
	15	57	5.1	113193	1	AF357202	AF357202 Streptomy
	16	56.8	5.1	15041	1	AE006991	AE006991 Mycobacte
	17	56	5.0	3803	1	MXCARQRS	X71062 M.xanthus g
c	18	55.8	5.0	41625	1	SCH24	AL049826 Streptomy
c	19	54	4.9	1506	6	AX120369	AX120369 Sequence
	20	53.2	4.8	14860	1	AE007093	AE007093 Mycobacte
	21	53.2	4.8	63033	1	MTV008	AL021246 Mycobacte
	22	53	4.8	1931	6	AR083152	AR083152 Sequence
c	23	52.2	4.7	749	14	NPORPT2	D13755 Multicapsid
c	24	52.2	4.7	131995	14	OPU75930	U75930 Orgyia pseu
	25	51	4.6	4026	1	SCO007313	AJ007313 Streptomy
	26	50	4.5	98002	2	AP003985	AP003985 Oryza sat
	27	49.4	4.5	1020	1	SAU59153	U59153 Streptomyce
c	28	49.4	4.5	10389	1	AE009479	AE009479 Brucella
c	29	49.2	4.4	109470	2	OSJN00062	AL606618 Oryza sat
	30	49	4.4	8046	1	AF049107	AF049107 Myxococcu
	31	48.6	4.4	303100	1	RME603646	AL603646 Rhizobium
c	32	48.6	4.4	323450	1	SME591790	AL591790 Sinorhizo
c	33	48.4	4.4	15311	1	AE007164	AE007164 Mycobacte

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 10:08:30 ; Search time 324 Seconds
(without alignments)
7708.229 Million cell updates/sec

Title: US-09-941-936A-1
Perfect score: 1109
Sequence: 1 tggaactggtgctccgttgt.....gctcttcgaggtgcgcttcc 1109

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1109	100.0	1109	24	AAD33874	Corynebacterium gl
c	2	1107.4	99.9	349980	22	AAH64966	C glutamicum codin
	3	577.4	52.1	579	22	AAH65249	C glutamicum codin
	4	161.4	14.6	4403765	22	AAI99683	Mycobacterium tube
	5	161.4	14.6	4411529	22	AAI99682	Mycobacterium tube
c	6	128	11.5	1603	22	AAF70989	C. glutamicum SRT
c	7	54	4.9	1506	22	AAH65250	C glutamicum codin
c	8	48.4	4.4	4403765	22	AAI99683	Mycobacterium tube
	9	46.8	4.2	65140	22	AAD17184	Streptomyces nous
	10	46.8	4.2	125401	22	AAD17186	Streptomyces nous
	11	46	4.1	4496	17	AAT58553	Streptomyces prist
	12	45.4	4.1	603	22	AAH68381	C glutamicum codin
	13	45.4	4.1	1211	24	AAL42355	Corynebacterium gl
	14	45.4	4.1	309400	22	AAH68534	C glutamicum codin
c	15	45	4.1	4411529	22	AAI99682	Mycobacterium tube
	16	44.6	4.0	37856	21	AAA11992	S. cellulosum DNA
	17	43.6	3.9	4689	21	AAZ87299	S. venezuelae macr
	18	43.6	3.9	13842	21	AAZ87297	S. venezuelae macr
	19	43.6	3.9	36778	21	AAZ87318	S. venezuelae pik
	20	43.6	3.9	37948	21	AAZ87285	S. venezuelae pik
	21	43.6	3.9	38506	21	AAA75633	Nucleotide sequenc
	22	43.6	3.9	38506	21	AAZ56001	Recombinant cosmid
c	23	43.4	3.9	689	24	ABQ29872	Oligonucleotide fo
	24	43.4	3.9	689	24	ABQ29873	Oligonucleotide fo
	25	43.2	3.9	11220	21	AAZ87298	S. venezuelae macr
	26	43	3.9	58857	21	AAA58471	Nucleotide sequenc
c	27	42.6	3.8	37856	21	AAA11992	S. cellulosum DNA
	28	42.4	3.8	1119	24	ABQ90343	M. capsulatus gene
	29	42.4	3.8	1119	24	ABQ90366	M. capsulatus gene
	30	41.6	3.8	3786	23	AAS54228	Pseudomonas aerugi
c	31	41.6	3.8	114955	20	AAX53491	Human adenosine A1
	32	41.4	3.7	528	22	AAF30761	Megalomicin polyke
c	33	40.8	3.7	953	24	ABQ45924	Oligonucleotide fo
	34	40.8	3.7	953	24	ABQ45925	Oligonucleotide fo
	35	40.6	3.7	2187	24	AAS95794	M. tuberculosis DN
	36	40.6	3.7	2190	22	AAA89042	Mycobacterium tube
	37	40.4	3.6	109519	22	AAS08693	Micromonospora DNA
c	38	40.2	3.6	876	22	AAF60769	Pseudomonas sp ABC
	39	40.2	3.6	20878	23	AAS59526	Propionibacterium
	40	40	3.6	1227	23	AAS51498	Pseudomonas aerugi
	41	39.8	3.6	1083	22	AAH68128	C glutamicum codin
	42	39.6	3.6	1473	21	AAA15140	DNA encoding an am
	43	39.4	3.6	1110	21	AAZ35221	Chromobacterium sp
	44	39.4	3.6	1110	24	ABK53024	Chromobacterium ge
	45	39.4	3.6	1639	16	AAQ92918	Chromobacterium es

ALIGNMENTS

RESULT 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 13:23:07 ; Search time 302 Seconds
(without alignments)
7575.721 Million cell updates/sec

Title: US-09-941-936A-1
Perfect score: 1109
Sequence: 1 tggaactggtgctccgttgt.....gctcttcgaggtgcgcttcc 1109

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1109	100.0	1109	11 US-09-941-936A-1	Sequence 1, Appli

Appl's published appl.

Nakagawa = ~~BB~~ USPAP 20020197605

c	2	1107.4	99.9	3309400	11	US-09-738-626-1	Sequence 1, Appli
	3	577.4	52.1	579	11	US-09-738-626-284	Sequence 284, App
	4	140.4	12.7	612	15	US-10-156-761-886	Sequence 886, App
	5	140.4	12.7	651	15	US-10-156-761-606	Sequence 606, App
c	6	140.4	12.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	7	54	4.9	1506	11	US-09-738-626-285	Sequence 285, App
	8	47.4	4.3	546	15	US-10-156-761-7271	Sequence 7271, Ap
c	9	45.6	4.1	520	15	US-10-184-644-332	Sequence 332, App
c	10	45.6	4.1	520	15	US-10-184-634-332	Sequence 332, App
	11	45.4	4.1	603	11	US-09-738-626-3416	Sequence 3416, Ap
	12	45.4	4.1	1211	11	US-09-942-935-1	Sequence 1, Appli
	13	45.4	4.1	6210	15	US-10-212-962-1	Sequence 1, Appli
	14	45.4	4.1	3309400	11	US-09-738-626-1	Sequence 1, Appli
	15	44.2	4.0	657	15	US-10-156-761-3104	Sequence 3104, Ap
	16	44.2	4.0	1440	15	US-10-156-761-6190	Sequence 6190, Ap
	17	44.2	4.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
	18	43.6	3.9	4689	11	US-09-861-289-34	Sequence 34, Appl
	19	43.6	3.9	4689	11	US-09-860-846-34	Sequence 34, Appl
	20	43.6	3.9	4689	12	US-09-988-384B-34	Sequence 34, Appl
	21	43.6	3.9	4689	12	US-09-836-821-34	Sequence 34, Appl
	22	43.6	3.9	13842	11	US-09-861-289-30	Sequence 30, Appl
	23	43.6	3.9	13842	11	US-09-860-846-30	Sequence 30, Appl
	24	43.6	3.9	13842	12	US-09-988-384B-30	Sequence 30, Appl
	25	43.6	3.9	13842	12	US-09-836-821-30	Sequence 30, Appl
	26	43.6	3.9	36778	11	US-09-861-289-5	Sequence 5, Appli
	27	43.6	3.9	36778	11	US-09-860-846-5	Sequence 5, Appli
	28	43.6	3.9	36778	12	US-09-836-821-5	Sequence 5, Appli
	29	43.6	3.9	37948	12	US-09-988-384B-5	Sequence 5, Appli
	30	43.6	3.9	38506	12	US-09-793-708-19	Sequence 19, Appl
	31	43.2	3.9	1125	15	US-10-156-761-6399	Sequence 6399, Ap
	32	43.2	3.9	11220	11	US-09-861-289-32	Sequence 32, Appl
	33	43.2	3.9	11220	11	US-09-860-846-32	Sequence 32, Appl
	34	43.2	3.9	11220	12	US-09-988-384B-32	Sequence 32, Appl
	35	43.2	3.9	11220	12	US-09-836-821-32	Sequence 32, Appl
	36	42.6	3.8	1647	15	US-10-156-761-4092	Sequence 4092, Ap
	37	42.6	3.8	6360	15	US-10-212-962-2	Sequence 2, Appli
	38	42.4	3.8	738	15	US-10-156-761-276	Sequence 276, App
	39	42.4	3.8	1149	15	US-10-156-761-6742	Sequence 6742, Ap
	40	42	3.8	591	15	US-10-156-761-6314	Sequence 6314, Ap
	41	41.8	3.8	405	15	US-10-156-761-3392	Sequence 3392, Ap
	42	41.6	3.8	3786	10	US-09-815-242-7865	Sequence 7865, Ap
	43	41.4	3.7	615	15	US-10-125-815-4	Sequence 4, Appli
c	44	41.2	3.7	426	11	US-09-960-352-12683	Sequence 12683, A
	45	41.2	3.7	1071	15	US-10-156-761-5553	Sequence 5553, Ap

ALIGNMENTS

RESULT 1

US-09-941-936A-1

; Sequence 1, Application US/09941936A

; Patent No. US20020146782A1

; GENERAL INFORMATION:

; APPLICANT: BATHE, Brigitte, et al.

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE sigD GENE

; FILE REFERENCE: 032301 WD 202

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 11:45:11 ; Search time 1896 Seconds
(without alignments)
9472.993 Million cell updates/sec

Title: US-09-941-936A-1
Perfect score: 1109
Sequence: 1 tggaactggtgctccgttggt.....gctcttcgaggtgcgcttcc 1109

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues.

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	53	4.8	925	17	CNS0091P			AL053013 Drosophil
	2	47.4	4.3	925	17	CNS0091P			AL053013 Drosophil
c	3	43.8	3.9	536	11	AY108186			AY108186 Zea mays
c	4	43.8	3.9	935	17	CNS006XK			AL066051 Drosophil
c	5	43.8	3.9	1101	17	CNS0039U			AL063935 Drosophil
c	6	43.6	3.9	997	17	AG073159			AG073159 Pan trogl
c	7	43.4	3.9	1230	14	BM809538			BM809538 AGENCOURT
c	8	42.6	3.8	695	17	AQ012113			AQ012113 8183H1B03
	9	42.2	3.8	384	12	BF598569			BF598569 sv19b02.y
	10	42.2	3.8	776	17	CNS010RY			AL099352 Drosophil
	11	42	3.8	561	13	BM302238			BM302238 MCA040C08
c	12	42	3.8	1169	14	BQ922913			BQ922913 AGENCOURT
	13	41.8	3.8	486	10	BE495363			BE495363 WHE1270_G
	14	41.8	3.8	654	13	BI953847			BI953847 HVSME001
c	15	41.8	3.8	878	17	AZ186896			AZ186896 SP_1008_A
c	16	41.6	3.8	766	10	BE659248			BE659248 GM700008B
c	17	41.4	3.7	671	13	BI463537			BI463537 603203649
	18	41.2	3.7	236	12	BG790943			BG790943 sae72a01.
	19	41.2	3.7	529	17	BH643714			BH643714 1008059F1
c	20	41.2	3.7	963	17	CNS04S6C			AL304797 Tetraodon
	21	41	3.7	550	10	BE402261			BE402261 CSB006B03
	22	41	3.7	550	14	BQ607895			BQ607895 BRY_3794
c	23	41	3.7	650	10	BE584886			BE584886 11-11H-ZO
	24	41	3.7	854	17	AG038993			AG038993 Pan trogl
	25	40.8	3.7	458	12	BG232108			BG232108 naf32h02.
c	26	40.8	3.7	466	9	AU173884			AU173884 AU173884
	27	40.8	3.7	805	14	BQ838243			BQ838243 WHE2908_B
	28	40.6	3.7	265	10	AW100223			AW100223 sd21c05.y
	29	40.6	3.7	421	10	BE660657			BE660657 323 GmaxS
c	30	40.6	3.7	434	12	BG356500			BG356500 EM1_23_C0
	31	40.6	3.7	559	13	BM522896			BM522896 sam99e08.
	32	40.6	3.7	580	14	BM892873			BM892873 sam49c08.
	33	40.6	3.7	584	10	AW233843			AW233843 sf26b04.y
c	34	40.6	3.7	918	17	AQ895329			AQ895329 HS_4832_A
	35	40.6	3.7	928	17	AG054567			AG054567 Pan trogl
	36	40.4	3.6	475	9	AU222993			AU222993 AU222993
	37	40.2	3.6	526	14	BQ471709			BQ471709 HV03D20r
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	42	40.2	3.6	611	13	BI776356			BI776356 EBem04_SQ
	43	40.2	3.6	625	14	BQ471300			BQ471300 HV02B04r
	44	40.2	3.6	685	12	BF627034			BF627034 HVSMEb000
	45	40.2	3.6	697	12	BF628719			BF628719 HVSMEb000

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 12:19:11 ; Search time 68 Seconds
(without alignments)
5001.537 Million cell updates/sec

Title: US-09-941-936A-1
Perfect score: 1109
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	161.4	14.6	4403765	4	US-09-103-840A-2			Sequence 2, Appli
	2	161.4	14.6	4411529	4	US-09-103-840A-1			Sequence 1, Appli
	3	53	4.8	1926	4	US-09-249-585A-4			Sequence 4, Appli
	4	53	4.8	1931	2	US-09-130-114-2			Sequence 2, Appli
c	5	48.4	4.4	4403765	4	US-09-103-840A-2			Sequence 2, Appli
	6	46	4.1	2220	4	US-08-765-907A-14			Sequence 14, Appl
	7	46	4.1	4496	4	US-08-765-907A-6			Sequence 6, Appli
c	8	45	4.1	4411529	4	US-09-103-840A-1			Sequence 1, Appli
	9	43.6	3.9	4689	4	US-09-105-537-34			Sequence 34, Appl
	10	43.6	3.9	13842	4	US-09-105-537-30			Sequence 30, Appl
	11	43.6	3.9	36778	4	US-09-105-537-5			Sequence 5, Appli

12	43.6	3.9	38506	3	US-09-320-878-19	Sequence 19, Appl
13	43.2	3.9	11220	4	US-09-105-537-32	Sequence 32, Appl
14	40.2	3.6	2219	3	US-08-510-646B-17	Sequence 17, Appl
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c 16	39	3.5	900	5	PCT-US95-04801-3	Sequence 3, Appli
c 17	38.6	3.5	1590	4	US-09-434-288-1	Sequence 1, Appli
18	38.4	3.5	521	4	US-09-643-597-324	Sequence 324, App
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20	38.4	3.5	28958	1	US-08-258-261B-6	Sequence 6, Appli
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34	37.8	3.4	390	4	US-09-197-649-7	Sequence 7, Appli
35	37.6	3.4	1685	6	5340934-1	Patent No. 5340934
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c 40	37.2	3.4	4394	3	US-08-471-869-1	Sequence 1, Appli
c 41	37.2	3.4	4394	4	US-09-342-563-1	Sequence 1, Appli
c 42	37.2	3.4	4394	5	PCT-US94-08267-1	Sequence 1, Appli
c 43	37.2	3.4	13987	2	US-08-804-227C-13	Sequence 13, Appl
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c 45	37.2	3.4	44377	2	US-08-804-198-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-103-840A-2

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

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; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765